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Gencore version 4.5

Result No.	Score	Query Match Length	DB ID	Description
c 1	24.6	63.1	178904 2	AL1354989 Homo sapi
c 2	24.6	63.1	184748 2	AL160051 Homo sapi
c 3	24.2	62.1	67982 2	AC068869 Homo sapi
c 4	24.2	62.1	107839 2	AC068869 Homo sapi
c 5	24.2	62.1	114478 2	AP000574 Homo sapi
c 6	24.2	62.1	123300 2	AP000406 Homo sapi
c 7	24.2	62.1	128206 2	AP001258 Homo sapi
c 8	24.2	62.1	225142 2	AP002358 Homo sapi
c 9	24.2	62.1	226020 2	AC007589 Homo sapi
c 10	24.6	63.1	195496 2	AL136014 Homo sapi
c 11	24.8	61.5	203257 9	AC013737 Homo sapi
c 12	23.8	61.0	1752 10	AF24362 Mus muscu
c 13	23.2	59.5	49743 2	AC017211 Drosophili
c 14	23.2	59.5	198721 2	AC010060 Drosophili
c 15	23.2	59.5	274585 3	AE003533 Drosophili
c 16	23.5	59.0	182127 2	AP001842 Mus muscu
c 17	23.5	59.0	12485 1	AE004962 Homo sapi
c 18	23.5	59.0	68790 9	HSJ287H17
c 19	23.5	59.0	136117 2	AC003700 Homo sapi
c 20	23.5	59.0	182127 2	AP001842 Homo sapi
c 21	23.5	59.0	184284 2	AC025582 Mus muscu
c 22	23.5	59.0	192110 2	AP004070 Oryza sativa
c 23	23.5	59.0	226899 2	AL159188 Homo sapi
c 24	22.8	58.5	1310192 9	AL157832 Human DNA
c 25	22.8	58.5	157058 2	AL157255 Homo sapi
c 26	22.8	58.5	187344 9	AL1354873 Human DNA
c 27	22.6	57.9	174253 2	AC025590 MNATD1G5
c 28	22.4	57.4	1148 9	HSIDTRAP HSU6268
c 29	22.4	57.4	1285 9	HSU6268 Human clone
c 30	22.4	57.4	1343 9	BC001902 Homo sapi
c 31	22.4	57.4	1362 9	BC000933 Homo sapi
c 32	22.4	57.4	1370 9	HSRNADH
c 33	22.4	57.4	1506 9	HSU0272 Human NADP+
c 34	22.4	57.4	18234 9	X14124 M. fascicula
c 35	22.4	57.4	191923 9	AC081886 Homo sapi
c 36	22.4	57.4	230516 9	HSU5211 Human clone
c 37	22.2	55.9	31600 2	AC019859 Drosophili
c 38	22.2	56.9	151162 9	AC003364 Human Chri
c 39	22.2	56.9	156508 3	AC027581 Drosophili
c 40	22.2	56.9	158648 2	Z08129 H. sapiens I
c 41	22.2	56.9	170609 3	AC007925 Drosophili
c 42	22.2	56.9	188090 9	AC011625 Homo sapi
c 43	22.2	56.9	306848 3	AE003464 Drosophili
c 44	22.2	56.4	123386 8	AC002131 Arabidops
c 45	22.2	56.4	134331 2	AL603727 Rattus no

## ALIGNMENTS

RESULT	1	AL134989/c	AL134989	178904 bp	DNA	HTG	02-AUG-2001
LOCUS							
DEFINITION							
PROGRESS	***,						
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							

AL134989 Human. HTGS PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

AL134989 Homo Sapiens chromosome 9 clone RP11-537H15, \*\*\* SEQUENCING IN

AL134989 PROGRESS \*\*\*, 2 unordered pieces.

AL134989.8 GI:15131225

AL134989.8 Human. HTGS PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

AL134989.8 Homo Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. I (bases 1 to 178904)

Chapman,J. Direct Submission

Submitted (01-Aug-2001) Sanger Centre, Hinxton, Cambridgeshire, C310 USA, UK. E-mail enquiries: hungquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 9, 2001 this sequence version replaced gi:14715324.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: BA53H15  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 177432 bases at least Q40  
 Consensus quality: 177660 bases at least Q30  
 Consensus quality: 177769 bases at least Q20  
 Insert size: 178804; sum-of-contigs  
 Insert size: 187738; 38.1% error; agarose-fp  
 Quality coverage: 16.40x in 020 bases; sum-of-contigs Quality coverage: 15.62x in 020 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
 \* 176743: contig of 176743 bp in length  
 \* 176844 176843: gap of 100 bp  
 \* 176844 178904: contig of 2061 bp in length.

**FEATURES**

**source**

- 1. 178904 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP11-57H15"  
 /clone\_id="RPCI-11.2"

1. 176743 fragment\_chain:1  
 /note="assembly\_fragment:03560  
 fragment\_chain:1  
 clone\_end:T7  
 vector\_side:left"  
 misc\_feature  
 /note="assembly\_fragment:06048  
 fragment\_chain:1"

**BASE COUNT** 52784 a 40958 c 39193 g 45869 t 100 others  
**ORIGIN**

Query Match 63.1%; score 24.6; DB 2; Length 178904;  
 Best Local Similarity 76.9%; Pid. No. 26;  
 Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 aggaatggcctggggcgttggaaatgccttatt 39  
 ||||| ||||| ||||| ||| ||||||||| |||  
 Db 164878 AGGGAAAGGCCTCTGGACATAGATATGCCCTGTGATT 164840

RESULT 2  
 ALL60051/C LOCUS ALL60051 184748 bp DNA HTG 27-JUN-2001  
 DEFINITION Homo sapiens chromosome 9 clone RP11-499G9, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces.  
 ACCESSION ALL60051  
 VERSION ALL60051.15  
 KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 184748)  
 AUTHORS Plumb,B.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerrequest@sanger.ac.uk  
 Web site: http://www.sanger.ac.uk  
 On Jun 28, 2001 this sequence version replaced gi:14251856.  
 ----- Genome Center

Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: Ba499G9  
 ----- Summary Statistics  
 Assembly Program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 179564 bases at least Q40  
 Consensus quality: 180555 bases at least Q30  
 Consensus quality: 181686 bases at least Q20  
 Insert size: 183048; sum-of-contigs  
 Insert size: 195118; 7.3% error; agarose-fp  
 Quality coverage: 9.04x in 020 bases; agarose-fp  
 Coverage: 9.76x in 020 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order in this sequence record is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
 \* 13081: contig of 13081 bp in length  
 \* 13181: gap of 100 bp  
 \* 13192 16206: contig of 3115 bp in length  
 \* 16297 16396: gap of 100 bp  
 \* 16397 57604: contig of 41208 bp in length  
 \* 57605 57704: gap of 100 bp  
 \* 57705 7998: contig of 22284 bp in length  
 \* 7998 8008: gap of 100 bp  
 \* 80089 95789: contig of 15701 bp in length  
 \* 95790 95889: gap of 100 bp  
 \* 95890 104909: contig of 9020 bp in length  
 \* 104910 105009: gap of 100 bp  
 \* 105010 117002: contig of 11993 bp in length  
 \* 117003 117102: gap of 100 bp  
 \* 117103 130858: contig of 13756 bp in length  
 \* 130859 130958: gap of 100 bp  
 \* 130959 140048: contig of 9890 bp in length  
 \* 140049 140148: gap of 100 bp  
 \* 140149 146391: contig of 6249 bp in length  
 \* 146398 146497: gap of 100 bp  
 \* 146498 148555: contig of 2062 bp in length  
 \* 148560 148659: gap of 100 bp  
 \* 148660 154236: contig of 5577 bp in length  
 \* 154237 154335: gap of 100 bp  
 \* 154337 156521: contig of 2187 bp in length  
 \* 156524 156623: gap of 100 bp  
 \* 156624 166567: contig of 9844 bp in length  
 \* 166568 166667: gap of 100 bp  
 \* 166668 173995: contig of 7278 bp in length  
 \* 173995 174095: gap of 100 bp  
 \* 174095 177011: contig of 2922 bp in length  
 \* 177018 177117: gap of 100 bp  
 \* 177118 181410: contig of 4293 bp in length  
 \* 181411 181510: gap of 100 bp  
 \* 181511 184748: contig of 3238 bp in length.

**FEATURES**

**source**

1. 13081 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP11-499G9"  
 /clone\_id="RPCI-11.2"

1. 13081

REFERENCE 1 (bases 1 to 67982)

REFERENCE AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

AUTHORS Homo sapiens chromosome 11, clone RP11-753E17

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 67982)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouloslavsky, L., Boukhalter, B., Brown, A., Burlett, G., Campopiano, A., Castle, A., Choevel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewart, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gindele, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heafield, A., Horton, L., Howard, J.C., Iliev, T., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Latocque, K., Lamazares, R., Landers, T., Lehozcy, J., Levine, R., Lieu, C., Liu, G., Locke, K., McDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McSheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Petersson, K., Pierre, N., Pisani, C., Polilaro, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thiermann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testayre, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT All repeats were identified using RepeatMasker; Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Project Information

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: sequence\_submissions@genome.wi.mit.edu  
Center: Genome Center  
Center project name: L9390  
Center clone name: 753\_E\_17

-----

\* NOTE: This record contains 93 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 646: contig of 646 bp in length  
\* 647 746: gap of 100 bp  
\* 747 1363: contig of 617 bp in length  
\* 1364 1463: gap of 100 bp  
\* 1464 2072: contig of 609 bp in length  
\* 2073 2172: gap of 100 bp  
\* 2173 2806: contig of 634 bp in length  
\* 2807 2906: gap of 100 bp  
\* 2907 3536: contig of 630 bp in length  
\* 3537 3636: gap of 100 bp  
\* 3637 4233: contig of 597 bp in length  
\* 4234 4333: gap of 100 bp  
\* 4334 4970: contig of 637 bp in length  
\* 4971 5070: gap of 100 bp  
\* 5071 5668: contig of 598 bp in length  
\* 5669 5768: gap of 100 bp  
\* 5769 6382: contig of 614 bp in length  
\* 6383 6482: gap of 100 bp  
\* 6483 7124: contig of 642 bp in length  
\* 7125 7224: gap of 100 bp  
\* 7225 7858: contig of 634 bp in length

RESULT 3

AC068869/C AC068869 67982 bp DNA HTG 10-MAY-2000

LOCUS Homo sapiens chromosome 11 clone RP11-753E17 map 11, LOW-PASS DEFINITION SEQUENCE SAMPLING.

ACCESSION AC068869 VERSION AC068869.1 GI:7767880 KEYWORDS HGVS\_PHASE0.

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo.

7859 7958: gap of 100 bp  
 \* 7959 8603: contig of 645 bp in length  
 \* 8604 8703: gap of 100 bp  
 \* 8704 9350: contig of 647 bp in length  
 \* 9351 9450: gap of 100 bp  
 \* 10065 10165: gap of 100 bp  
 \* 10166 10791: contig of 632 bp in length  
 \* 10798 10897: gap of 100 bp  
 \* 10898 11522: contig of 625 bp in length  
 \* 11523 11622: gap of 100 bp  
 \* 11623 12251: contig of 629 bp in length  
 \* 12252 12351: gap of 100 bp  
 \* 12352 12988: contig of 637 bp in length  
 \* 12989 13088: gap of 100 bp  
 \* 13089 13708: contig of 620 bp in length  
 \* 13709 13908: gap of 100 bp  
 \* 13809 14413: contig of 665 bp in length  
 \* 14454 14553: gap of 100 bp  
 \* 14554 15193: contig of 640 bp in length  
 \* 15194 15293: gap of 100 bp  
 \* 15294 15925: contig of 632 bp in length  
 \* 15926 16025: gap of 100 bp  
 \* 16026 16601: contig of 615 bp in length  
 \* 16641 16740: gap of 100 bp  
 \* 16741 17378: contig of 638 bp in length  
 \* 17379 17478: gap of 100 bp  
 \* 17479 18084: contig of 606 bp in length  
 \* 18085 18188: gap of 100 bp  
 \* 18185 18825: contig of 641 bp in length  
 \* 18826 18925: gap of 100 bp  
 \* 18926 19545: contig of 620 bp in length  
 \* 19546 19645: gap of 100 bp  
 \* 19646 20303: contig of 658 bp in length  
 \* 20304 20403: gap of 100 bp  
 \* 20404 21035: contig of 632 bp in length  
 \* 21036 21135: gap of 100 bp  
 \* 21136 21797: contig of 661 bp in length  
 \* 21797 21896: gap of 100 bp  
 \* 21897 22333: contig of 637 bp in length  
 \* 22334 22633: gap of 100 bp  
 \* 22634 23256: contig of 623 bp in length  
 \* 23257 23356: gap of 100 bp  
 \* 23357 24007: contig of 651 bp in length  
 \* 24008 24107: gap of 100 bp  
 \* 24108 24751: gap of 100 bp in length  
 \* 24852 25580: contig of 629 bp in length  
 \* 24851 25580: gap of 100 bp  
 \* 25581 26192: contig of 612 bp in length  
 \* 26193 26292: gap of 100 bp  
 \* 26293 26899: contig of 607 bp in length  
 \* 26900 26999: gap of 100 bp  
 \* 27000 27609: contig of 610 bp in length  
 \* 27610 27709: gap of 100 bp  
 \* 27710 28433: contig of 624 bp in length  
 \* 28334 28433: gap of 100 bp  
 \* 28434 29067: contig of 634 bp in length  
 \* 29068 29167: gap of 100 bp  
 \* 29168 29822: contig of 655 bp in length  
 \* 29823 29922: gap of 100 bp  
 \* 30690 31333: contig of 643 bp in length  
 \* 31334 31433: gap of 100 bp  
 \* 31434 32076: contig of 643 bp in length  
 \* 32077 32176: gap of 100 bp  
 \* 32177 32917: contig of 641 bp in length  
 \* 32818 32917: gap of 100 bp  
 \* 32918 33544: contig of 627 bp in length  
 \* 33545 33644: gap of 100 bp  
 \* 33645 34293: contig of 649 bp in length  
 \* 34294 34393: gap of 100 bp

Query Match 62.1%; Score 24.2; DB 2; Length 67982;  
 Best Local Similarity 78.4%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY	1	agagatggccttggcccttggaaatggccctta 37
Db	63244	AGTAGGTTGGCAATGTTGCTAGGAATGGCCTCTGA 63208

RESULT 4

AP000574/c AP000574 DNA

LOCUS AP000574 107839 bp HGTG

DEFINITION Homo sapiens chromosome 11 clone CMB9-49B9 map 11q12, WORKING DRAFT

SEQUENCE, 9 unordered pieces.

ACCESSION AP000574

VERSION AP000574.2

KEYWORDS HTG, HTGS-PHASE1, HTGS-DRAFT

SOURCE Homo sapiens DNA, clone:CMB9-49B9.

ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 107839)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 107,839 genomic DNA of 11q12

REFERENCE Published Only in Database (1999) In press

AUTHORS 2 (bases 1 to 107839)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

TITLE  
JOURNAL  
Submitted (08-OCT-1999) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail: hattori@gsc.riken.go.jp, Tel:81-42-778-9924)

## COMMENT

On May 31, 2000 this sequence version replaced gi:6997466.

----- Genome Center

Center: RIKEN Genomic Sciences Center(GSC)

Center code: RIKEN

Web site: http://hgp-gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

/Project Information

Center project name: HumDraftII

Center clone name: CMB9-49B9

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-Terminator EP-amerham;

Assembly program: Phrap; version 0.990329

Consensus quality: 01252 bases at least Q40

Consensus quality: 105065 bases at least Q30

Consensus quality: 106437 bases at least Q20

Insert size: 107039; sum-of-contigs

Quality coverage: 4.56x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

Sequence updated (26-May-2000)  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
 1 24330 contig of 24330 bp in length  
 24431 46451 contig of 22021 bp in length  
 46552 58483 contig of 11932 bp in length  
 58584 69637 contig of 11054 bp in length  
 69738 82347 contig of 12610 bp in length  
 82448 91301 contig of 8854 bp in length  
 91402 98707 contig of 72306 bp in length  
 98808 105638 contig of 6831 bp in length  
 105739 107839 contig of 2101 bp in length

RESULT	5
AP000489/c	
LOCUS	AP000489 11478 bp DNA
DEFINITION	Homo sapiens chromosome 11 clone CMB9-7F5 map 11q13, WORKING DRAFT
ACCESSION	Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
VERSION	Q4
KEYWORDS	GI:8118775
SOURCE	HGP; PHASEL; HGVS_DRAFT.
ORGANISM	Homo sapiens DNA, clone:CMB9-7F5.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bakes 1 to 114478)
REFERENCE	Fujiyama,A., Yada,T., Totoki,Y., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H., and Sakaki,Y.
JOURNAL	Homino Sapiens 114,478 genomic DNA of 11q13
REFERENCE	Published Only in DataBase (1999) In press
AUTHORS	2 (bases 1 to 114478)
REFERENCE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H., and Sakaki,Y.
JOURNAL	Submitted (13 SEP-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail: hattori@gsc.riken.go.jp, Tel:81-42-778-9924, URL:http://hgp-gsc.riken.go.jp/, Fax:81-42-778-9924)
COMMENT	On May 31, 2000 this sequence version replaced gi:6997459.
----- Genome Center	
Center: RIKEN Genomic Sciences Center(GSC)	
Web site: http://hgp-gsc.riken.go.jp/	
Contact: hattori@gsc.riken.go.jp	
Center Project name: HumDraftII	
Center clone name: CMB9-7F5	
----- Summary Statistics	
Sequencing vector: PCR products; 100% of reads	
Chemistry: Dye-terminator EP-amerham; 100% of reads	

FEATURES  
source  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

Assembly program: phrap; version 0.990329  
 Consensus quality: 109628 bases at least Q40  
 Consensus quality: 112052 bases at least Q30  
 Consensus quality: 113108 bases at least Q20  
 Insert size: 113878; sum-of-contigs

Quality coverage: 6.65x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1. 58724 contig of 58724 bp in length  
 58825 83984 contig of 23160 bp in length  
 84085 95379 contig of 11295 bp in length  
 95480 105075 contig of 9596 bp in length  
 105176 111400 contig of 6225 bp in length  
 111501 113338 contig of 1838 bp in length  
 113439 114478 contig of 1040 bp in length

Sequence updated (04-Nov-1999)

Sequence updated (26-May-2000)

\* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1. 58724: contig of 58724 bp in length  
 \* 58725 58824: gap of 100 bp  
 \* 58825 83984: contig of 25160 bp in length  
 \* 83985 84084: gap of 100 bp  
 \* 84085 95379: contig of 11295 bp in length  
 \* 95380 95473: gap of 100 bp  
 \* 95480 105075: contig of 9596 bp in length  
 \* 105076 105175: gap of 100 bp  
 \* 105176 111400: contig of 6225 bp in length  
 \* 111401 111500: gap of 100 bp  
 \* 111501 113338: contig of 1838 bp in length  
 \* 113339 113438: gap of 100 bp  
 113439 114478: contig of 1040 bp in length.

**FEATURES**

source

1. .114478  
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 /chromosome="11"  
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 /clone="CMB9-7F5"
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 /note="assembly\_fragment" .83984
1. .95379  
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 /note="assembly\_fragment"  
 /note="assembly\_fragment" .105075
1. .111400  
 /note="assembly\_fragment clone\_end:T7 vector\_side:left" .48085  
 /note="assembly\_fragment" .95379
1. .111501  
 /note="assembly\_fragment clone\_end:SP6 vector\_side:right" .113338  
 /note="assembly\_fragment" .114478
1. .23225  
 /note="assembly\_fragment" .23593

BASE COUNT 33314 a 23225 g 33746 t 600 others  
 ORIGIN

Query Match 62.1%; score 24.2; DB 2; length 114478;  
 Best Local Similarity 78.4%; Pred. No. 37;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 54667 AGTAGGTGCAATGTCCTAGGAATGGCCCTCTGA 54631

DEFINITION HMG-21D9 map 11q12, WORKING DRAFT

ACCESSION AP000405

VERSION AP000406 4 GL-9927270

KEYWORDS HMG; HMG\_PHRSE; HMG\_DRAFT

SOURCE Homo sapiens DNA, clone:CMB9-21D9

ORGANISM Homo sapiens

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 123300)  
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fulljama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Homo sapiens, 123,300 genomic DNA of 11q12

JOURNAL Published Only in DataBase (1999) In press

REFERENCE 2 (bases 1 to 123300)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fulljama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 E-mail:hattori@scg.riken.go.jp, URL:http://hg.p.gsc.riken.go.jp/,  
 Tel: 81-42-778-9923, Fax: 81-42-778-9924

COMMENT On Aug 26, 2000 this sequence version replaced gi:8118745.

JOURNAL Direct Submission

REFERENCE Submitted (27-AUG-1999) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-15-1 Kita-saito, Sagamihara, Kanagawa 228-8555, Japan

CONTACT: hattori@gsc.riken.go.jp/  
 Center code: RIKEN  
 Web site: http://hg.p.gsc.riken.go.jp/  
 Center project name: HumanDraft1  
 Center clone name: CMB9-21D9

COMMENT Summary statistics

Sequencing vector: PCR products; 100% of reads  
 Chemistry: dye-terminator  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 121846 bases at least Q40  
 Consensus quality: 122507 bases at least Q30  
 Consensus quality: 122832 bases at least Q20  
 Insert size: 123000; sum-of-contigs

Quality coverage: 13.07x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1. 61533 contig of 61533 bp in length  
 61634 10681 contig of 45248 bp in length  
 10692 119565 contig of 12584 bp in length  
 119666 12300 contig of 365 bp in length.

\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1. 61533: contig of 61533 bp in length  
 \* 61534 61633: gap of 100 bp  
 \* 61634 10681: contig of 45248 bp in length  
 \* 10682 106981: gap of 100 bp



JOURNAL  
Published Only in DataBase (2000) In press  
REFERENCE  
2 (bases 1 to 225142)  
AUTHORS  
Hattori,M., Ishii,T., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suenri-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:hattori@gsc.riken.go.jp; URL: http://hgps.gsc.riken.go.jp/;  
Tel:81-45-531111, Fax:81-45-503-9170)

COMMENT

On Jan 13, 2001 this sequence version replaced 91:8131622.

Center: RIKEN Genomic Sciences Center(GSC)  
Center code: RIKEN  
Web site: http://hgps.gsc.riken.go.jp/  
Contact: hattori@gsc.riken.go.jp

Project Information

Project name: Rundraft11

Center clone name: RP11-1036E20

Summary Statistics

Sequencing vector: PCR products: 100% of reads

Chemistry: Dye-terminator ET-amersham: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 219245 bases at least Q40

Consensus quality: 222418 bases at least Q30

Consensus quality: 223448 bases at least Q20

Insert size: 22394; sum-of-contigs

Quality coverage: 8.03x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 55748 contig of 55748 bp in length

55849 81106 contig of 25526 bp in length

81207 105043 contig of 21837 bp in length

105144 129107 contig of 21964 bp in length

149114 contig of 19907 bp in length

149215 165516 contig of 16302 bp in length

165617 182204 contig of 16588 bp in length

182305 192999 contig of 10695 bp in length

193100 203328 contig of 10229 bp in length

203429 208865 contig of 5437 bp in length

208966 216574 contig of 7609 bp in length

216675 222800 contig of 6126 bp in length

222901 225142 contig of 2242 bp in length.

225142 clone of 11

/clone="RP11-1036E20"

1. 55748 /note="assembly\_fragment" 193100 . 203328 /note="assembly\_fragment" 149215 . 165516 /note="assembly\_fragment" 165617 . 182204 /note="assembly\_fragment" 182305 . 192999 /note="assembly\_fragment" 193100 . 203328 /note="assembly\_fragment" 165617 . 182204 /note="assembly\_fragment" 203429 . 208865 /note="assembly\_fragment" 208966 . 216574 /note="assembly\_fragment" 216675 . 222800 /note="assembly\_fragment" 222901 . 225142 /note="assembly\_fragment" 225142 clone\_end:T7 vector\_side:left" 208865 a 46820 c 47221 g 66847 t 1200 others

BASE COUNT 63054 a 46820 c 47221 g 66847 t

ORIGIN

Query Match 62.18; Score 24.2; DB 2; Length 225142;

Best Local Similarity 78.4%; Pred. No. 37;

Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agagatggcctgtggcccttggaaatggccctta 37

Db 188212 AGTAGGTGGCAATGTGCTAGAAATGCCCTGA 188248

RESULT 9

AC087689 AC087689 226020 bp DNA

LOCUS AC087689 226020 bp DNA

DEFINITION Homo sapiens chromosome 11 clone RP11-1036E20 map 11, WORKING DRAFT

SEQUENCE 9 unordered pieces.

ACCESSION AC087689

VERSION AC087689.3 GI:14210561

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 226020)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 11, clone RP11-1036E20

REFERENCE 2 (bases 1 to 226020)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

	Source																																												
Barna, N., Bastien, V., Boguslavskyi, L., Camarata, J., Campopiano, A., Chopeley, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArllano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, J., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gindele, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K., Lamarares, R., Landers, T., Lehozciak, J., Levine, R., Liu, G., MacLean, C., McDonald, P., Marquis, N., Matthews, C., McCarty, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'bonnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, R., Schuback, R., Seaman, S., Severi, P., Sougnez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamaas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	1. 226020 /note="assembly_fragment" /note="Homo sapiens" /note="clone_end;SP6 /note="chromosome" 11 /map="11" /clone="RP11-1036E20" /clone 11b="RP11-11 Human Male BAC" 1. .2472 /note="assembly_fragment" /note="clone_end;SP6 /note="vector_side:left" 2573. .3289 /note="assembly_fragment" /note="assembly_fragment" 3390. .4086 /note="assembly_fragment" 4187. .5709 /note="assembly_fragment" /note="assembly_fragment" 5810. .1792 /note="assembly_fragment" 18073. .43215 /note="assembly_fragment" 45316. .92283 /note="assembly_fragment" 92384. .156424 /note="assembly_fragment" 156525. .226020 /note="assembly_fragment" clone_end;T/ vector_side:right" clone_end;T/ vector_side:right"																																												
TITLE	Direct Submission																																												
JOURNAL																																													
COMMENT	Submitted (15 JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 27, 2001 this sequence version replaced gi 31323260. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>																																												
Center: Whitehead Institute/ MIT Center for Genome Research																																													
Center code: WIBR																																													
Web site: <a href="http://www.seq.wi.mit.edu">http://www.seq.wi.mit.edu</a>																																													
Contact: sequence_submissions@genome.wi.mit.edu																																													
----- Project Information																																													
Center project name: L12345																																													
Center clone name: 1056_E_20																																													
----- Summary Statistics																																													
Sequencing vector: plasmid; n/a; 100% of reads																																													
Chemistry: Dye-terminator																																													
Big Dye;																																													
Assembly program: phrap;																																													
version 0.960731																																													
Consensus quality: 224743 bases at least Q40																																													
Consensus quality: 222976 bases at least Q30																																													
Consensus quality: 223564 bases at least Q20																																													
Insert size: 224000; agarose-fp																																													
Insert size: 225220; sum-of-contigs																																													
Quality coverage: 8.7 in Q20 bases; agarose-fp																																													
Quality coverage: 8.7 in Q20 bases; sum-of-contigs																																													
-----																																													
* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.																																													
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.																																													
* 1 2472: contig of 2472 bp in length																																													
* 2473 2572; gap of 100 bp																																													
* 2573 3289; contig of 717 bp in length																																													
* 3290 3389; gap of 100 bp																																													
* 3390 4086: contig of 597 bp in length																																													
* 4087 4186; gap of 100 bp																																													
* 4187 5709: contig of 1523 bp in length																																													
* 5710 5809; gap of 100 bp																																													
* 5810 1792; contig of 12163 bp in length																																													
* 17973 18072; gap of 100 bp																																													
* 18073 45215: contig of 27143 bp in length																																													
* 45216 45315; gap of 100 bp																																													
* 45316 92283: contig of 46968 bp in length																																													
* 5810 92383; gap of 100 bp																																													
* 92384 156424: contig of 64041 bp in length																																													
* 156425 156524: gap of 100 bp																																													
* 156525 226020: contig of 69496 bp in length.																																													
Location/Qualifiers																																													
-----																																													
BASE COUNT	66670	ORIGIN	a 47794 C 46268 g 64486 t 802 others	RESULT	10	AU360214/c		LOCUS	195496 bp DNA	DEFINITION	Homo sapiens chromosome 10 clone RP11-533N7, *** S	VERSION	AL360214	VERSION	AL360214.18 GI:15131258	KEYWORDS	HTG; HTGS_PHASEL; HTGS_ACTIVERVERIN; HTGS_DRAFT; HTGS_SOURCE human.	ORGANISM	Homo sapiens	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae	AUTHORS	Chapman, J.	TITLE	Direct Submission	JOURNAL	Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridge, UK. E-mail enquiries: humquery@sanger.ac.uk	COMMENT	requests: clonerequest@sanger.ac.uk On Aug 9, 2001 this sequence version replaced gi 11323260 ----- Project Information	Center project name: bu533N7		----- Summary Statistics		Assembly program: XGAP4; version 4.5		Sequencing vector: plasmid; L08752; 100% of reads		Chemistry: Dye-terminator		Big Dye;		100% of reads		Consensus quality: 194004 bases at least Q40	
ORIGIN	a 47794 C 46268 g 64486 t 802 others																																												
RESULT	10																																												
AU360214/c																																													
LOCUS	195496 bp DNA																																												
DEFINITION	Homo sapiens chromosome 10 clone RP11-533N7, *** S																																												
VERSION	AL360214																																												
VERSION	AL360214.18 GI:15131258																																												
KEYWORDS	HTG; HTGS_PHASEL; HTGS_ACTIVERVERIN; HTGS_DRAFT; HTGS_SOURCE human.																																												
ORGANISM	Homo sapiens																																												
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae																																												
AUTHORS	Chapman, J.																																												
TITLE	Direct Submission																																												
JOURNAL	Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridge, UK. E-mail enquiries: humquery@sanger.ac.uk																																												
COMMENT	requests: clonerequest@sanger.ac.uk On Aug 9, 2001 this sequence version replaced gi 11323260 ----- Project Information																																												
Center project name: bu533N7																																													
----- Summary Statistics																																													
Assembly program: XGAP4; version 4.5																																													
Sequencing vector: plasmid; L08752; 100% of reads																																													
Chemistry: Dye-terminator																																													
Big Dye;																																													
100% of reads																																													
Consensus quality: 194004 bases at least Q40																																													









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Query Match Similarity 59.5%; Score 23.2; DB 3; Length 274585;  
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 QY 8 ggccttggggccttggaaatggccct 35  
 .Db 138449 GGCCttGGGGCAAGGCATGGCTCT 138422

Search completed: January 29, 2002, 21:25:11.  
 Job time: 1819 sec